

REMARKS

The specification, sequence listing and claims 1, 4, 12, 22, 24, 25, 34, 35, 44, 45, 46, 47, 48, 52, 53, 54, and 56 have been amended to include recitation of new nucleotide sequences SEQ ID NOS:35 and 37 and amino acid sequences SEQ ID NO:36 and 38.

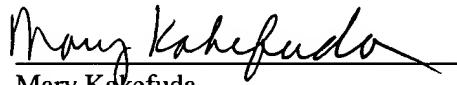
New matter has been added by this amendment, prior to the expiration of the priority year (Aug. 1, 2001).

The amendments are designated above and below using underlining where the text has been added.

For the convenience of the examiner, a substitute specification, a marked-up copy of the original specification, and substitute sequence listing are submitted herewith.

No fee is believed due with this amendment. If any fees are required, please charge them to the Deposit Account No. 50-1744 (in the name of Syngenta).

Respectfully submitted,



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Version of Specification and Claims Showing Amendments

IN THE SPECIFICATION:

Please amend the specification to read as follows:

On page 3, second paragraph:

-- In one aspect, the present invention encompasses novel methods for controlling gene silencing in a plant cell. The present invention encompasses the suppression of gene silencing or the increase in gene silencing in plants. In a preferred embodiment, this is achieved by altering the expression in the plant cell of a nucleotide sequence encoding a polypeptide comprising a 3'-5' exonuclease domain. In another embodiment, the nucleotide molecule encodes a polypeptide comprising exonuclease activity, preferably having 3'-5' RNA exonuclease activity. Preferably, the polypeptide comprises a 3'-5' exonuclease domain. More preferably, the 3'-5' exonuclease domain is an RNase D related domain. In another preferred embodiment, the polypeptide is identical or substantially similar to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:22, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16 SEQ ID NO:18, SEQ ID NO:24, SEQ ID NO:36 or SEQ ID NO:38. Preferably, the nucleotide sequence is identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15 SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37. Most preferably, the nucleotide sequence is identical or substantially identical to SEQ ID NO:23.--

On page 3, fourth paragraph:

--In a preferred embodiment, the expression of a nucleotide sequence encoding a polypeptide comprising a 3'-5' exonuclease domain is altered by altering its transcription or translation. Reduced expression is for example obtained by expressing in the plant cell a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15 SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 in sense orientation, or a portion thereof; or expressing in the plant cell a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11 SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 in anti-sense orientation, or a portion thereof; or expressing in the plant cell a sense RNA of a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11 SEQ ID NO:13, [or] SEQ ID NO:23,

SEQ ID NO:35 or SEQ ID NO:37 or a portion thereof, and an anti-sense RNA of said nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 or a portion thereof, wherein said sense and said anti-sense RNAs are capable of forming a double-stranded RNA molecule; or expressing in said plant cell a ribozyme capable of specifically cleaving a messenger RNA transcript encoded by a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 or modifying by homologous recombination in said plant cell at least one chromosomal copy of a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 or of a regulatory region thereof; or expressing in said plant cell a zinc finger protein that is capable of binding to a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 or to a regulatory region thereof; or introducing into said plant cell a chimeric oligonucleotide that is capable of modifying at least one chromosomal copy of a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 or a regulatory region thereof. Preferably, the expression of the sequence is altered by insertional mutagenesis, point mutation or deletion mutagenesis of the genomic copy of a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 or a regulatory region thereof. Alternatively, the sequence has a mutation due to rearrangement.--

On page 5, fourth paragraph:

--The present invention also encompasses an expression cassette comprising a nucleic acid molecule of the present invention comprising a nucleotide sequence encoding a polypeptide comprising a 3'-5' exonuclease domain, or complement thereof. Preferably, the expression cassette comprises a nucleic acid molecule comprises a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37--

On page 6, third paragraph:

-- An isolated nucleic acid molecule comprising a nucleotide sequence encoding a polypeptide comprising a 3'-5' exonuclease domain, and wherein the polypeptide is identical or substantially similar to an amino acid sequence of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:22, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, [or] SEQ ID NO:24, SEQ ID NO:36 or SEQ ID NO:38 or complements thereof. Preferably, the polypeptide is identical or substantially --

On page 7, first paragraph:

-- similar to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6 or SEQ ID NO:22. More preferably, the polypeptide is identical or substantially similar to SEQ ID NO:2 or SEQ ID NO:24. In another preferred embodiment, the nucleotide sequence is identical or substantially similar to a nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37. Preferably, the nucleotide sequence is identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, or SEQ ID NO:23. More preferably, the nucleotide sequence is substantially similar to SEQ ID NO:1. Most preferably, the nucleotide sequence is identical or substantially similar to SEQ ID NO:23. In another preferred embodiment, the 3'-5' exonuclease domain preferably comprises an RNase D related domain. Preferably, the polypeptide comprises 3'-5' exonuclease activity, and most preferably, 3'-5' RNA exonuclease activity. In yet another preferred embodiment, the nucleotide sequence is derived from a plant.--

On page 7, second paragraph:

-- The present invention further provides an isolated recombinant nucleic acid molecule comprising a nucleotide sequence encoding a polypeptide encoded by the amino acid sequence identical or substantially similar to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:22, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, [or] SEQ ID NO:24, SEQ ID NO:36 or SEQ ID NO:38, or complements thereof. More preferably, the recombinant nucleic acid molecules comprise the nucleotide sequence of SEQ ID NO:23 or complement thereof. The recombinant nucleic acid molecule is operatively linked to a promoter functional in a cell. Preferably, the promoter is functional in a plant cell. --

On page 7, third paragraph:

-- An isolated and substantially purified polypeptide comprising an amino acid sequence identical or substantially similar to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:22, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16 SEQ ID NO:18, [or] SEQ ID NO:24, SEQ ID NO:36, or SEQ ID NO:38. Preferably, the polypeptide comprises the amino acid sequence of SEQ ID NO:24. Alternatively, the polypeptide consists of the amino acid sequence of SEQ ID NO:24.--

On page 8, third paragraph:

-- A cell comprising the nucleic acid or recombinant nucleic acid molecule of the present invention, and a cell comprising the expression cassette of the present invention. Preferably, the cell is a plant cell. In a preferred embodiment, the nucleotide sequence of the present invention is expressed in said plant cell. In another preferred embodiment, the expression cassette promoter is a constitutive promoter, an inducible promoter, a tissue-specific promoter or a developmentally-regulated promoter. In another preferred embodiment, the expression cassette or recombinant nucleic acid molecule is stably integrated in the genome of the plant cell. In yet another preferred embodiment, the plant cell comprises an endogenous nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37. Preferably, the endogenous nucleotide sequence is identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5 SEQ ID NO:21, or SEQ ID NO:23. More preferably, the endogenous nucleotide sequence is identical or substantially similar to SEQ ID NO:1. Most preferably, the nucleotide sequence is identical or substantially similar to SEQ ID NO:23. Preferably, the expression of said endogenous nucleotide sequence in said plant cell is altered.--

On page 9, first paragraph:

-- A plant cell comprising an endogenous nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 and wherein said plant cell comprises a mutation in said endogenous nucleotide sequence, or in a regulatory region thereof. Preferably, said mutation is due to the insertion of a nucleic acid molecule into said endogenous nucleotide sequence or into a regulatory region thereof, wherein the expression of said endogenous nucleotide sequence in said plant is altered. Preferably, the endogenous--

On page 9, fifth paragraph:

-- A plant cell or plant capable of expressing a sense RNA molecule of a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 and an anti-sense RNA molecule of said nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 wherein said sense and said anti-sense RNA molecules are capable of forming a double-stranded RNA molecule. An advantage of the invention is that the expression in said plant cell of an endogenous nucleotide sequence of said plant cell that is substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 is reduced.--

On page 10, third paragraph:

-- A method for altering the expression of an endogenous nucleotide sequence that is identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 in a plant cell or plant comprising the step of: altering the transcription or translation of said endogenous nucleotide sequence in said plant cell or plant.

In a preferred embodiment, wherein altering the transcription or translation of said endogenous nucleotide sequence in said plant cell or plant comprises the step of:

a) expressing in said plant cell a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 or a portion thereof, in sense orientation; or

b) expressing in said plant cell a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 or a portion thereof, in anti-sense orientation; or

c) expressing in said plant cell a sense RNA of a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a portion thereof, and an anti-sense RNA of said nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a portion thereof, wherein said sense and said anti-sense RNAs are capable of forming a double-stranded RNA molecule; or

d) expressing in said plant cell a ribozyme capable of specifically cleaving a messenger RNA transcript encoded by a nucleotide sequence identical or substantially --

On page 11, first paragraph:

--similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37; or

e) modifying by homologous recombination in said plant cell at least one chromosomal copy of the nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 or of a regulatory region thereof; or

f) expressing in said plant cell a zinc finger protein that is capable of binding to a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or to a regulatory region thereof; or

g) introducing into said plant cell a chimeric oligonucleotide that is capable of modifying at least one chromosomal copy of the nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 or a regulatory region thereof.--

On page 11, second paragraph:

-- A method for altering the expression of an endogenous nucleotide sequence that is as described or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 in

a plant cell comprising introducing into said plant cell a means for altering the transcription or translation of said endogenous nucleotide sequence in said plant cell.--

On page 11, third paragraph:

-- A method for altering the expression of a nucleotide sequence of interest in a plant cell or plant comprising the steps of:

a) altering the expression in said plant cell or plant of an endogenous nucleotide sequence of said plant cell that is identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37; and

b) introducing into said plant cell a nucleic acid molecule comprising said nucleotide sequence of interest, wherein the expression of said nucleotide sequence of interest in said plant cell or plant is altered.--

On page 12, first paragraph:

-- a) expressing in said plant cell a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a portion thereof, in sense orientation; or

b) expressing in said plant cell a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a portion thereof, in anti-sense orientation; or

c) expressing in said plant cell a sense RNA of a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a portion thereof, and an anti-sense RNA of said nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a portion thereof, wherein said sense and said anti-sense RNAs are capable of forming a double-stranded RNA molecule; or

d) expressing in said plant cell a ribozyme capable of specifically cleaving a messenger RNA transcript encoded by a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 or

e) modifying by homologous recombination in said plant cell at least one chromosomal copy of the nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or of a regulatory region thereof; or

f) expressing in said plant cell a zinc finger protein that is capable of binding to a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or to a regulatory region thereof; or

g) introducing into said plant cell a chimeric oligonucleotide that is capable of modifying at least one chromosomal copy of the nucleotide identical or sequence substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 or a regulatory region thereof--

On page 13, first paragraph:

-- A method for stabilizing the expression of a nucleotide sequence of interest in a plant cell comprising:

a) altering the expression in a plant cell of an endogenous nucleotide sequence of said plant cell that encodes a polypeptide comprising a 3'-5' exonuclease domain, and wherein said polypeptide is identical or substantially similar to an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:22, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, [or] SEQ ID NO:24, SEQ ID NO:36 and SEQ ID NO:38; and

b) introducing into said plant cell a nucleotide sequence of interest, --

On page 13, third paragraph through page 14:

-- Preferably, the polypeptide has 3'-5' RNA exonuclease activity. Preferably, the 3'-5' exonuclease domain is an RNase D related domain. Preferably, the endogenous nucleotide sequence is identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5,

SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37.

Preferably, the expression of said endogenous nucleotide sequence is altered by:

a) expressing in said plant cell a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a portion thereof, in sense orientation; or

b) expressing in said plant cell a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a portion thereof, in anti-sense orientation; or

c) expressing in said plant cell a sense RNA of a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a portion thereof, and an anti-sense RNA of said nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a portion thereof, wherein said sense and said anti-sense RNAs are capable of forming a double-stranded RNA molecule; or

d) expressing in said plant cell a ribozyme capable of specifically cleaving a messenger RNA transcript encoded by a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37; or

e) expressing in said plant cell an aptamer specifically directed to a polypeptide identical or substantially similar to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:22, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, [or] SEQ ID NO:24, SEQ ID NO:36 or SEQ ID NO:38; or

f) modifying by homologous recombination in said plant cell at least one chromosomal copy of the nucleotide sequence identical or substantially similar to SEQ ID--

On page 15, first partial paragraph:

-- NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or of a regulatory region thereof; or

g) expressing in said plant cell a zinc finger protein that is capable of binding to a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or to a regulatory region thereof; or

h) introducing into said plant cell a chimeric oligonucleotide that is capable of modifying at least one chromosomal copy of the nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a regulatory region thereof.--

On page 15, first paragraph:

-- The present invention further provides:

A method for identifying a compound capable of interacting with a polypeptide comprising a 3'-5' exonuclease domain comprising:

a) combining a polypeptide comprising the amino acid sequence set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:22, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, [or] SEQ ID NO:24, SEQ ID NO:36 or SEQ ID NO:38, or a homolog thereof, and a compound to be tested for the ability to interact with said polypeptide, under conditions conducive to interaction; and

b) selecting a compound from step (a) that is capable of interacting with said polypeptide.--

On page 15, second paragraph:

-- Preferably, the polypeptide is encoded by a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37.--

On page 16, amend the sequence listing to read as follows:

---- SEQ ID NO:9 nucleotide sequence corresponding to GenPept accession AAD26968

SEQ ID NO:10 GenPept accession AAD26968

SEQ ID NO:11 nucleotide sequence corresponding to GenPept accession AAC25931

SEQ ID NO:12 GenPept accession AAC25931

SEQ ID NO:13 nucleotide sequence corresponding to GenPept accession AAF98185

SEQ ID NO:14 GenPept accession AAF98185

SEQ ID NO:15 nucleotide sequence corresponding to GenPept accession CAA80137
SEQ ID NO:16 GenPept accession CAA80137
SEQ ID NO:17 nucleotide sequence corresponding to GenPept accession AAF06162
SEQ ID NO:18 GenPept accession AAF06162
SEQ ID NO:19 Oligonucleotide 3' specific primer
SEQ ID NO:20 Oligonucleotide pD991 primer
SEQ ID NO:21 corrected nucleotide sequence corresponding to corrected GenPept
accession AAC42241
SEQ ID NO:22 corrected GenPept accession AAC42241
SEQ ID NO:23 nucleotide sequence of cDNA encoding a polypeptide comprising a
RNase D related domain from *Arabidopsis thaliana*
SEQ ID NO:24 amino acid sequence of polypeptide comprising a RNase D related domain
from *Arabidopsis thaliana*
SEQ ID NO:25 oligonucleotide T-DNA specific primer LB1
SEQ ID NO:26 oligonucleotide T-DNA specific primer LB2
SEQ ID NO:27 oligonucleotide T-DNA specific primer LB3
SEQ ID NO:28 oligonucleotide arbitrary degenerate primer AD3
SEQ ID NO:29 oligonucleotide primer 36851TD#3
SEQ ID NO:30 gene-specific oligonucleotide primer L22F4F
SEQ ID NO:31 gene-specific oligonucleotide primer F22L4R
SEQ ID NO:32 oligonucleotide primer AtWRN CDS F
SEQ ID NO:33 oligonucleotide primer AtWRN-RT-R
SEQ ID NO:34 oligonucleotide primer AtWRN CDS R
SEQ ID NO:35 nucleotide sequence corresponding to GenPept accession AAG50917
SEQ ID NO:36 GenPept accession AAG50917
SEQ ID NO:37 nucleotide sequence corresponding to GenPept accession BAB11227
SEQ ID NO:38 GenPept accession BAB11227--

On page 23, first paragraph:

-- The inventors of the present invention are the first to screen for plant nucleotide sequences encoding a polypeptide comprising a 3'-5' exonuclease domain, and to successfully identify such nucleotide sequences. This is carried out according to the methods disclosed in Example 1. The amino acid sequences and corresponding nucleotide sequences identified using the method and algorithms disclosed in Example 1 are set forth in SEQ ID NO:1-14, and 35-38 and briefly

described as follows. An amino acid sequence predicted from a genomic sequence from *Arabidopsis thaliana* is found in GenBank under accession #CAB36851 and is set forth in SEQ ID NO:2. The corresponding nucleotide sequence is found in BAC F18A5, GenBank accession number AL035528.2. An amino acid sequence predicted from a genomic sequence from *Arabidopsis thaliana* is found in GenBank under accession #AAD25623 and is set forth in SEQ ID NO:4. The corresponding nucleotide sequence is found in BAC F20D21, GenBank accession number AC005287.4. An amino acid sequence predicted from a genomic sequence from *Arabidopsis thaliana* is found in GenBank under accession #AAC69936 and is set forth in SEQ ID NO:6. The corresponding nucleotide sequence is found in *Arabidopsis thaliana* chromosome II section 181 of 255, GenBank accession number AC005700.2. An amino acid sequence predicted from a genomic sequence from *Arabidopsis thaliana* is found in GenBank under accession #AAC42241 and is set forth in SEQ ID NO:8. The corresponding nucleotide sequence is found in *Arabidopsis thaliana* chromosome II section 145 of 255, GenBank accession number AC005395.2. An amino acid sequence predicted from a genomic sequence from *Arabidopsis thaliana* is found in GenBank under accession #AAD26968 and is set forth in SEQ ID NO:10. The corresponding nucleotide sequence is found in *Arabidopsis thaliana* chromosome II section 197 of 255, GenBank accession number AC007135.7. An amino acid sequence predicted from a genomic sequence from *Arabidopsis thaliana* is found in GenBank under accession #AAC25931 and is set forth in SEQ ID NO:12. The corresponding nucleotide sequence is found in *Arabidopsis thaliana* chromosome II section 182 of 255, GenBank accession number AC004681.2. An amino acid sequence predicted from a genomic sequence from *Arabidopsis thaliana* is found in GenBank under accession #AAF98185 and is set forth in SEQ ID NO:14. The corresponding nucleotide sequence is found in BAC F17F8, GenBank accession number AC000107.2. An amino acid sequence predicted from a genomic sequence from *Arabidopsis thaliana* is found in GenBank under accession # AAG50917 and is set forth in SEQ ID NO:36. The corresponding nucleotide sequence is found in BAC F14G9, GenBank accession number AC069159. An amino acid sequence predicted from a genomic sequence from *Arabidopsis thaliana* is found in GenBank under accession # BAB11227 and is set forth in SEQ ID NO:38. The corresponding nucleotide sequence is found in BAC K16H17, GenBank accession number AB016884.--

On page 24, second paragraph,

--Further, the present invention provides for nucleic acid molecules encoding a full length nucleotide sequence encoding a polypeptide comprising a 3'-5' exonuclease domain of SEQ ID

NO:24 as was cloned from *Arabidopsis thaliana* as set forth in Examples 2-3. The invention also provides a nucleic acid molecule comprising or having the sequence identical or substantially similar to the nucleotide sequence of SEQ ID NO:23 or complements thereof. The inventors of the present invention predicted a 3'-5' exonuclease domain between about amino acid positions 129 and 287 in the amino acid sequence set forth in SEQ ID NO:2. The inventors of the present invention also predicted that the amino acid sequence between about amino acid positions 136 and 271 in SEQ ID NO:4 is comprised in a 3'-5' exonuclease domain, that the amino acid sequence between about amino acid positions 76 and 210 in SEQ ID NO:6 is comprised in a 3'-5' exonuclease domain, that the amino acid sequence between about amino acid positions 46 and 199 in SEQ ID NO:22 is comprised in a 3'-5' exonuclease domain, that the amino acid sequence between about amino acid positions 57 and 193 in SEQ ID NO:10 is comprised in a 3'-5' exonuclease domain, that the amino acid sequence between about amino acid positions 66 and 202 in SEQ ID NO:12 is comprised in a 3'-5' exonuclease domain, that the amino acid sequence between about amino acid positions 380 and 538 in SEQ ID NO:36 is comprised in a 3'-5' exonuclease domain, that the amino acid sequence between about amino acid positions 30 and 193 in SEQ ID NO:38 is comprised in a 3'-5' exonuclease domain. The inventors of the present invention also predict that the amino acid sequence between about amino acid positions 129 and 282 in SEQ ID NO:24 comprises a 3'-5' exonuclease domain. --

On page 24, fourth paragraph:

-- Thus, the present invention discloses a nucleotide sequence encoding a polypeptide identical or substantially similar to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:22, SEQ ID NO:10, SEQ ID NO:12, [or] SEQ ID NO:14, SEQ ID NO:36 or SEQ ID NO:38. Preferably, the polypeptide is identical or substantially similar to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, or SEQ ID NO:22. More preferably, the polypeptide is identical or substantially similar to SEQ ID NO:2. Most preferably, the polypeptide is identical or substantially similar to the amino acid sequence of SEQ ID NO:24.--

On page 24, fifth paragraph through page 25:

-- Preferably, the nucleotide sequence is identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11 SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37. More preferably, the nucleotide sequence is substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, or SEQ ID NO:21. Yet more preferably, the nucleotide sequence is identical or substantially similar to SEQ ID NO:1.

Most preferably, the nucleotide sequence is identical or substantially similar to SEQ ID NO:23. --

On page 25, third paragraph:

-- Based on Applicants' disclosure of the present invention, nucleotide sequences encoding polypeptides identical or substantially similar to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, [or] SEQ ID NO:24, SEQ ID NO:36 or SEQ ID NO:38 are isolated, preferably from the genome of any desired plant. For example, all or part of the nucleotide sequence set forth in SEQ ID NO:1 is used as a probe that selectively hybridizes to other nucleotide sequences present in a population of cloned genomic DNA fragments or cDNA fragments (i.e. genomic or cDNA libraries) from a chosen source organism. Such techniques include hybridization screening of plated DNA libraries (either plaques or colonies; see, *e.g.* Sambrook *et al.*, "Molecular Cloning", eds., Cold Spring Harbor Laboratory Press. (1989)) and amplification by PCR using oligonucleotide primers corresponding to sequence domains conserved among such polypeptides (see, *e.g.* Innis *et al.*, "PCR Protocols, a Guide to Methods and Applications", Academic Press (1990)). For example, oligonucleotide primers corresponding to a portion of a 3'-5' exonuclease domain are used. These methods are particularly well suited to the isolation of nucleotide sequences from organisms closely related to the organism from which the probe sequence is derived. Isolation of such a nucleic acid molecule of the present invention, in particular SEQ ID NO:23, is described in Example 7. --

On page 44, third paragraph:

-- VIII. Polypeptides encoded by the nucleic acid molecules.

The present invention provides polypeptides encoded by the nucleic acid molecules of the invention and variants thereof. These polypeptides are exemplified by those encoded by the nucleotide sequences of SEQ ID NOS: 2, 4, 6, 22, 18, 12, 14, [and] 24, 36 and 38; polypeptides encoded by nucleic acid sequences having at least 70% sequence similarity to the sequences of SEQ ID NOS: 1, 3, 5, 21, 9, 11, 13, [or] 23, 35 or 37 and variants and mutants thereof. Preferably, the isolated and substantially purified polypeptides are identical or substantially similar to the amino acid sequence of SEQ ID NO:24.--

On page 47, first paragraph:

-- The 3'-5' exonuclease domain consists of three sequence motifs termed Exo I, Exo II, and Exo III (Moser *et al.* (1997) *Nucl. Acids Res.* 25:5110-5118). These motifs are clustered around the active site and contain four negatively charged amino acids that serve as ligands for the two metal

ions necessary for catalysis in addition to a catalytically active tyrosine. The presence of these amino acids in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:22, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, and SEQ ID NO:18, and their position in the corresponding amino acid sequences is indicated in Table 1 below. The positions of the exo I, exo II, and exo III motifs in these amino acid sequences is shown in Table 2.

Method 3

Additional Arabidopsis genes that encode proteins with 3'-5' exonuclease domains are identified starting from the experimentally determined cDNA sequence for the gene encoded by SEQ ID NO:1. This protein sequence (SEQ ID NO:24) is identified as described in Example 6 (see below). A BLASTp search (Altschul, S.F. et al. (1997) *Nucleic Acids Res.* 25:3389-3402) with SEQ ID NO:24 as the query reveals that there are several predicted Arabidopsis proteins with E values less than 1E-03. From this group of Arabidopsis proteins, a HMM search is performed with each protein as a query compared to the HMM database of PFAM models (version 6.4) on a TimeLogic DeCypher machine. Two Arabidopsis proteins (AAG50917 (SEQ ID NO:36) and BAB11227 (SEQ ID NO:38)) are identified that were not identified by methods 1 and 2 earlier. The nucleotide sequences corresponding to AAG50917 and BAB11227 are SEQ ID NO:35 and SEQ ID NO:37, respectively. These proteins have E values from the HMM search that are below 1E-01 and likely to be significant. For comparison, the E-values for all the Arabidopsis proteins identified in Example 1 are shown in the third column in Tables 1 and 2 as recalculated with the same HMM program, PFAM model, and computer server.--

On page 47, Table 1:

-- Table 1:

Accession #	E-value HMM	E-value HMM**	exo I	exo II	exo III
AAD25623 (SEQ ID NO:4)	4.6E-54	<u>2.7E-67</u>	D140, E142	D199	Y264, D268
AAC69936 (SEQ ID NO:6)	1.5E-44	<u>5.8E-82</u>	D80, E82	D138	Y203, D207
CAB36851 (SEQ ID NO:2)	2.0E-04	<u>9.8E-12</u>	D133, E135	D194	Y263, D267
AAC42241* (SEQ ID NO:22)	1.5E-01	<u>7.6E-27</u>	D50, E52	D108	A192, D196
AAD26968 SEQ ID NO:10)	5.1E+00	=	D61, Q63	D118	Q186, D190
AAC25931 (SEQ ID NO:12)	-	=	G70, Q72	D127	Q195, D199
AAF98185 (SEQ ID NO:14)	-	=	-	-?	Y60, R64
<u>AAG50917 (SEQ ID NO:36)</u>	-	<u>6.6E-11</u>	<u>D384, E386</u>	<u>D449</u>	<u>Y531, D535</u>
<u>BAB11227 (SEQ ID NO:38)</u>	-	<u>2.4E-14</u>	<u>D34, E36</u>	<u>D104</u>	<u>Y186, D190</u>
CAA80137 (SEQ ID NO:16)	-	=	D435, E437	D503	Y585, D589
AAF06162 (SEQ ID NO:18)	-	=	D82, E84	D143	Y212, D216

*: using corrected sequence because 5' end is missing due to incorrect annotation, so that exo 1 may be present.

**: HMM PFAM analysis done as per Method 3 of Example 1

exo I, II, & III motifs defined as in Figure 6 of Mian (1997) *Nucleic Acids Res* 25:3187--

On page 47-48, Table 2:

-- Table 2:

Accession #	E-value HMM	E-value HMM**	exo I	exo II	exo III
AAD25623 (SEQ ID NO:4)	4.6E-54	<u>2.7E-67</u>	136-145	191-206	261-271
AAC69936 (SEQ ID NO:6)	1.5E-44	<u>5.8E-82</u>	76-85	130-135	200-210
CAB36851 (SEQ ID NO:2)	2.0E-04	<u>9.8E-12</u>	129-138	186-201	260-270
AAC42241* (SEQ ID NO:22)	1.5E-01	<u>7.6E-27</u>	46-55	100-115	189-199
AAD26968 (SEQ ID NO:10)	5.1E+00	-	57-66	110-125	183-193
AAC25931 (SEQ ID NO:12)	-	-	66-75	119-134	192-202
AAF98185 (SEQ ID NO:14)	-	-	-	-	57-67
<u>AAG50917 (SEQ ID NO:36)</u>		<u>6.6E-11</u>	<u>380-389</u>	<u>441-456</u>	<u>528-538</u>
<u>BAB11227 (SEQ ID NO:38)</u>		<u>2.4E-14</u>	<u>30-39</u>	<u>96-111</u>	<u>183-193</u>
CAA80137 (SEQ ID NO:16)	-	-	431-440	495-510	582-592
AAF06162 (SEQ ID NO:18)	-	-	78-87	135-150	209-219

*: using corrected sequence because 5' end is missing due to incorrect annotation, so that exo 1 may be present.

**: HMM PFAM analysis done as per Method 3 of Example 1--

On page 53, third paragraph:

-- Alternatively, a nucleotide sequence set forth in any one of SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, [or] SEQ ID NO:17, SEQ ID NO:35 or SEQ ID NO:37 is included in a construct as described above and is used for overexpression of a polypeptide comprising a 3'-5' exonuclease domain.--

IN THE CLAIMS:

1. (amended) An isolated nucleic acid molecule comprising a nucleotide sequence encoding a polypeptide comprising a 3'-5' exonuclease domain, and wherein said polypeptide is identical or substantially similar to an amino acid sequence of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:22, SEQ ID NO:10, SEQ ID NO:12, [or] SEQ ID NO:24, SEQ ID NO:36 or SEQ ID NO:38.

4. (amended) An isolated nucleic acid molecule comprising a nucleotide sequence [=] identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21,

SEQ ID NO:9 , SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37.

12. (amended) An expression cassette comprising a nucleic acid molecule comprising a nucleotide sequence encoding a polypeptide comprising a 3'-5' exonuclease domain, and wherein said polypeptide is identical or substantially similar to an amino acid sequence of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:22, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:16 , SEQ ID NO:18,[or] SEQ ID No:24, SEQ ID NO:36 or SEQ ID NO:38, a promoter, and a terminator.

22. (amended) The plant cell according to claim 20, further comprising an endogenous nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37.

25. (amended) A plant cell comprising an endogenous nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, and wherein said plant cell comprises a mutation in said endogenous nucleotide sequence, or in a regulatory region thereof.

34. (amended) A plant cell capable of expressing a sense RNA molecule of a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, and an anti-sense RNA molecule of said nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, wherein said sense and said anti-sense RNA molecules are capable of forming a double-stranded RNA molecule.

35. (amended) The plant cell according to claim 34, wherein the expression of the endogenous nucleotide sequence of said plant cell that is identical or substantially similar to SEQ

ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 is reduced.

44. (amended) A method for altering the expression in a plant cell or plant of an endogenous nucleotide sequence encoding a polypeptide comprising a 3'-5' exonuclease domain, wherein said polypeptide is identical or substantially similar to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:22, SEQ ID NO:10, SEQ ID NO:12, [or] SEQ ID NO:24, SEQ ID NO:36 or SEQ ID NO:38 comprising the step of:

altering the transcription or translation of said endogenous nucleotide sequence in said plant cell or plant.

45. (amended) The method according to claim 44, wherein altering the transcription or translation of said endogenous nucleotide sequence in the plant cell or plant comprises the step of:

a) expressing in said plant cell a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 or a portion thereof, in sense orientation; or

b) expressing in said plant cell a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a portion thereof, in anti-sense orientation; or

c) expressing in said plant cell a sense RNA of a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a portion thereof, and an anti-sense RNA of said nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a portion thereof, wherein said sense and said anti-sense RNAs are capable of forming a double-stranded RNA molecule; or

d) expressing in said plant cell a ribozyme capable of specifically cleaving a messenger RNA transcript encoded by a nucleotide sequence identical or substantially

similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37; or

e) modifying by homologous recombination in said plant cell at least one

chromosomal copy of the nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or of a regulatory region thereof; or

f) expressing in said plant cell a zinc finger protein that is capable of binding to a

nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or to a regulatory region thereof; or

g) introducing into said plant cell a chimeric oligonucleotide that is capable of modifying at least one chromosomal copy of the nucleotide sequence

identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a regulatory region thereof.

46. (amended) A method for altering the expression of an endogenous nucleotide sequence that is identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 in a plant cell or plant comprising the step of introducing into said plant cell a means for altering the transcription or translation of said endogenous nucleotide sequence in said plant cell.

47. (amended) A method for altering the expression of a nucleotide sequence of interest in a plant cell or plant comprising the steps of:

a) altering the expression in said plant cell or plant of an endogenous nucleotide sequence of said plant cell that is identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37; and

b) introducing into said plant cell or plant a nucleic acid molecule comprising said nucleotide sequence of interest, wherein the expression of said nucleotide sequence of interest in said plant cell or plant is altered.

48. (amended) The method according to claim 47, wherein step a) comprises:

- expressing in said plant cell or plant a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a portion thereof, in sense orientation; or
- expressing in said plant cell or plant a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a portion thereof, in anti-sense orientation; or
- expressing in said plant cell or plant a sense RNA of a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a portion thereof, and an anti-sense RNA of said nucleotide sequence substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a portion thereof, wherein said sense and said anti-sense RNAs are capable of forming a double-stranded RNA molecule; or
- expressing in said plant cell or plant a ribozyme capable of specifically cleaving a messenger RNA transcript encoded by a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37; or
- modifying by homologous recombination in said plant cell or plant at least one chromosomal copy of the nucleotide sequence substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or of a regulatory region thereof; or
- expressing in said plant cell or plant a zinc finger protein that is capable of binding to a nucleotide sequence substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or to a regulatory region thereof; or

g) introducing into said plant cell or plant a chimeric oligonucleotide that is capable of modifying at least one chromosomal copy of the nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a regulatory region thereof.

52. (amended) A method for stabilizing the expression of a nucleotide sequence of interest in a plant cell or plant comprising the steps of:

- a) obtaining a plant cell or plant having altered expression in a plant cell of an endogenous nucleotide sequence of said plant cell or plant that encodes a polypeptide comprising a 3'-5' exonuclease domain, and wherein said polypeptide is identical or substantially similar to an amino acid sequence of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:22, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, [or] SEQ ID NO:24, SEQ ID NO:36 or SEQ ID NO:38; and
- b) introducing into said plant cell or plant a nucleotide sequence of interest, wherein the expression of said nucleotide sequence of interest in said plant cell is stabilized as compared to the expression of said nucleotide sequence of interest in a plant cell or plant lacking said first expression cassette.

53. (amended) The method according to claim 52, wherein said endogenous nucleotide sequence is identical or substantially similar to a nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37.

54. (amended) The method according to claim 52, wherein the expression of said endogenous nucleotide sequence is altered by:

- a) expressing in said plant cell a nucleotide sequence substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a portion thereof, in sense orientation; or
- b) expressing in said plant cell a nucleotide sequence substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a portion thereof, in anti-sense orientation; or

- c) expressing in said plant cell a sense RNA of a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a portion thereof, and an anti-sense RNA of said nucleotide sequence substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a portion thereof, wherein said sense and said anti-sense RNAs are capable of forming a double-stranded RNA molecule; or
- d) expressing in said plant cell a ribozyme capable of specifically cleaving a messenger RNA transcript encoded by a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or
- e) expressing in said plant cell an aptamer specifically directed to a polypeptide substantially similar to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:22, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, [or] SEQ ID NO:24, SEQ ID NO:36 or SEQ ID NO:38, or
- f) modifying by homologous recombination in said plant cell at least one chromosomal copy of the nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or of a regulatory region thereof; or
- g) expressing in said plant cell a zinc finger protein that is capable of binding to a nucleotide sequence substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or to a regulatory region thereof; or
- h) introducing into said plant cell a chimeric oligonucleotide that is capable of modifying at least one chromosomal copy of the nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a regulatory region thereof.

56. (amended) A method for identifying a compound capable of interacting with a polypeptide comprising a 3'-5' exonuclease domain comprising:

a) combining a polypeptide comprising the amino acid sequence set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:22, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, [or] SEQ ID NO:24, SEQ ID NO:36 or SEQ ID NO:38, or a homolog thereof, and a compound to be tested for the ability to interact with said polypeptide, under conditions conducive to interaction; and

b) selecting a compound from step (a) that is capable of interacting with said polypeptide.

IN THE SEQUENCE LISTING:

Please amend the sequence listing to add SEQ ID NOS; 35-38 as follows:

<210> 35

<211> 1749

<212> DNA

<213> Arabidopsis thaliana

<400> 35

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TACCTACTCA	AAGAATGCTA	TAAACATGGT	AGCTTGAAGG	CAACAAAAAA	GTTCCAAGCT	180
TTACAGTATC	AAGTCATCG	AGTTCTAGCT	AATAAACCTC	AACCAGGACC	TGCTACTTTC	240
ATTATTAATT	GTCTCACTTT	ACTTCCTTTA	TTTGGGGTAT	ATGGTGAAGG	CTTTAGTCAT	300
TTAGTTATC	CGCTCTTCG	CCGCTCTTT	AAAACAGTAT	CTGAACCAAC	TAGTGAAGAA	360
GATATTGTT	TGGCGAGAAA	GCTACTGCT	CAGTTCTTCC	TTGCTACTGT	TGGTGGATCT	420
TTAACTTATG	ATGAGAAGGT	TATGGTGCAT	ACTCTTAGAG	TGTTTGATGT	GAGGTTAACT	480
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AATGCGTTTC	TGGAACAATA	CATTCTGAC	TTGATCAAGT	CGAAATCTT	CATGACGGCT	600
GTGACTCTGT	TAGAGCATT	CTCTTCCGT	TTCCCTGGAG	AAACTTTCT	TCAACAAATG	660
GTTGAGGATA	AAAATTCCA	AGCTCAGAG	AGATGGGCTA	CCTTCATGGG	AAGGCCAAGT	720
TTATGCATTC	TTGTTCAAGA	GTATGGCTCA	AGGAATATGC	TAAAGCAGGC	CTATAATATC	780
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GCTCTGAAGG	TTCTAGCAGA	AAAAGCATGT	TGGGATGTTG	CTGAAATTAA	GACAAAAGGT	900
GATAGACAGC	TTCTGAAGTA	TCTGGTATAC	TTGGCAGTGG	AACTGGATA	CTTGGAGAAG	960
GTTGATGAAC	TGTGCGATCG	ATATTCACTT	CAAGGGCTGC	CAAAAGCACG	AGAGGCTGAG	1020
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TTTCAATGTG	ACATCAAGCA	GTGGCGCTT	TCATATGGGG	ATTTGAAATG	TTTCGAGCGA	1440
TACGACATGT	TGCTAGACAT	TCAAAATGTT	TTAATGAAC	CATTTGGTGG	TTTAGCAGGA	1500
CTAACGAAGA	AAATATGGG	AGTGTCTTTG	AAACAAACAA	GACGCAATAG	CGACTGGGAA	1560
CAAAGCCCTT	TGAGCCAGAA	TCACGTTGAG	TATGCTGCTC	TTGATGCTGC	AGTGTGATT	1620
CACATATTTC	GCCATGTTCG	CGATCATCCT	CCACATGACA	GTAGTTCAGA	GACAACCCAG	1680
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<211> 582

<212> PRT

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<400> 36

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Ile Ile Asn Cys Leu Thr Leu Leu Pro Leu Phe Gly Val Tyr Gly Glu
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Gly Phe Ser His Leu Val Ile Ser Ala Leu Arg Arg Phe Phe Lys Thr
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165 170 175

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210 215 220

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Arg Lys Ala Thr Ser Phe Leu Glu Gly Cys Arg Val Val Gly Ile Asp		
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CACGCCACGG ATGTCCTCGA TGTCCTTCCTC ATTGATTGTA GTTCGATTCA TCTTCCATCG 240
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CTGGACATCT CTCTCTCAAA GGAACCTCAA TGTAGTGATT GGTCATATCG TCCCTCTACA 540
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Val Trp Glu Leu Leu Asn Asp Met Phe Val Ser Pro Asp Val Leu Lys
85 90 95

Leu Gly Phe Arg Phe Lys Gln Asp Leu Val Tyr Leu Ser Ser Thr Phe
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465 470 475 480

His Gln Leu Tyr Trp Glu Gly Thr Gln Tyr His Asn Ala Val Gln Lys
485 490 495

Phe Met Glu Val Cys Lys Leu Ser Glu
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